

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Inze, Dirk
Segers, Gerda
De Veylder, Lieven
Mironov, Vladimir
- (ii) TITLE OF INVENTION: METHOD AND MEANS FOR MODULATING
PLANT CELL CYCLE PROTEINS AND THEIR USE IN PLANT
CELL GROWTH AND CONTROL
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Nixon Peabody LLP
 - (B) STREET: 990 Stewart Avenue
 - (C) CITY: Garden City
 - (D) STATE: New York, New York
 - (E) ZIP: 11530
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP PCT/EP98/01522
 - (B) FILING DATE: 13-MAR-1998
 - (A) APPLICATION NUMBER: EP 97.200.765.2
 - (B) FILING DATE: 14-MAR-1997

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCTCTGAGAG AGAA ATG GGT CAG ATC CAA TAC TCC GAG AAA TAC TTC GAT	50
Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp	
1 5 10	
GAC ACT TTC GAA TAC AGG CAC GTC GTT CTT CCT CCT GAA GTC GCT AAA	98
Asp Thr Phe Glu Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys	
15 20 25	
CTT CTT CCA AAG AAT CGT CTT CTC TCC GAA AAC GAA TGG CGA GCG ATA	146
Leu Leu Pro Lys Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile	
30 35 40	
GGA GTG CAG CAA AGC CGC GGA TGG GTA CAT TAC GCG GTT CAT CGA CCT	194
Gly Val Gln Gln Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro	
45 50 55 60	
GAG CCG CAC ATA ATG CTA TTC AGG AGG CCT CTT AAC TAT CAG CAG CAG	242
Glu Pro His Ile Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln	
65 70 75	
CAG GAG AAT CAA GCT CAG AAC ATG CTT GTT AAG T GAATCATTAT	286
Gln Glu Asn Gln Ala Gln Asn Met Leu Val Lys	
80 85	
CATCACCTGA GTAAGAATGT TATATGCAAC AATTCTATGA GTATTGGTTT ATGTTTCTTG	346
TAAACATGGT TTGAATCTTT GTGGTTATGG ATGAATATGT GAGAGTTGGT TTGTTGAACA	406
ACTTCTATGT AATGTTAGTC TTGGTTCTAA TGTCATCTTC TGCTTCTC	454

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGGTCAGA TCCAATACTC CGAGAAATAC TTCGATGACA CTTTCGAATA CAGGTAAAGC	60
TCTTCAATCT CGCTTCTTCT TCCTCCAATT TTCACTCTCA CTTCTCTAAT CGTAATCGAT	120
CGATACAGGC ACGTCGTTCT TCCTCCTGAA GTCGCTAAAC TTCTTCCAAA GAATCGTCTT	180
CTCTCCGAAG TAAGTTTTTT TCCGCATTGT TCTCTGATTT CTGATTCTAA ATCCTTCGAT	240
TAGATCATCG AAGACTATGA AAATTGTG CTCTTAAGAA ATTAAGTTTG GGAAAAATCG	300

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AAAAAGAGAT CGTTTAGGTT TAGGATTTGA ATCTTTGCTC TGAATCCAAA TTGCAACTGT      360
TACGATTTTG AATCTTTGCT TTGGGATTTT GTAAGGTTTA GTGATAAAGA GATTTTAGAC      420
ATTTGTGTTG TGCAATCTCT TCAATGTTGT ATTGATTGGT GGTGATGGTA AAAATGTTTG      480
GAATTTCGAA GAACGAATGG CGAGCGATAG GAGTGCAGCA AAGCCGCGGA TGGGTACATT      540
ACGCGGTTCA TCGACCTGAG CCGCACATAA TGCTATTCAG GAGGCCTCTT AACTATCAGC      600
AGCAGCAGGA GAATCAAGCT CAGAACATGC TTGTTAAGTG AATCATTATC ATCACCTGAG      660
TAAGAATGTT ATATGCAACA GATCTATGAG TATTGG                                696

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
1           5           10           15
Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
20           25           30
Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
35           40           45
Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
50           55           60
Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln Gln Glu Asn Gln
65           70           75           80
Ala Gln Asn Met Leu Val Lys
85

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
1 5 10 15

Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
20 25 30

Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
35 40 45

Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
50 55 60

Met Leu Phe Arg Arg Pro Leu Asn
65 70